

WEST Search History

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update

DATE: Monday, November 08, 2004

Hide?	Set Name	Query	Hit Count
		<i>DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI,TDBD; PLUR=YES; OP=AND</i>	
<input type="checkbox"/>	L1	dam.clm.	3925
<input type="checkbox"/>	L2	L1 and salmonel\$.clm.	12

END OF SEARCH HISTORY

First Hit Fwd Refs

L2: Entry 11 of 12

File: USPT

May 7, 2002

DOCUMENT-IDENTIFIER: US 6383496 B1

TITLE: Recombinant vaccines comprising immunogenic attenuated bacteria having RPOS positive phenotype

CLAIMS:

3. The method according to claim 1 wherein the bacteria is a strain of Salmonella.
4. The method according to claim 3 wherein the Salmonella is a strain of *S. typhi*.
5. The method according to claim 4 wherein the one or more inactivating mutations are in a gene selected from the group consisting of a pab gene, a pur gene, an aro gene, asd, a dap gene, nadA, pncB, galE, pmi, fur, rpsL, ompR, htrA, hemA, cdt, cya, crp, dam, phoP, phoQ, rfc, poxA, galU, metL, methH, mviA, sodC, recA, ssrA, ssrB, sirA, sirB, sirC, inv, hila, hilC, hild, rpoE, flgM, tonB, and slyA.
10. A carrier bacteria according to claim 8 wherein the bacteria is a Salmonella.
11. A carrier bacteria according to claim 10 wherein the Salmonella is an *S. typhi*.
12. The carrier bacteria according to claim 11 wherein the one or more inactivating mutations are in a gene selected from the group consisting of a pab gene, a pur gene, an aro gene, asd, a dap gene, nadA, pncB, galE, pmi, fur, rpsL, ompR, htrA, hemA, cdt, cya, crp, dam, phoP, phoQ, rfc, poxA, galU, metL, methH, mviA, sodC, recA, recA, ssrA, ssrB, sirA, sirB, sirC, inv, hila, hilC, hild, rpoE, flgM, tonB, and slyA.
17. The composition according to claim 15 wherein the bacteria is a Salmonella.
18. The composition according to claim 17 whreein the Salmonella is an *S. typhi*.
19. The composition according to claim 18 wherein the one or more inactivating mutations are in a gene selected from the group consisting of a pab gene, a pur gene, an aro gene, asd, a dap gene, nadA, pncB, galE, pmi, fur, rpsL, ompR, htrA, hemA, cdt, cya, crp, dam, phoP, phoQ, rfc, poxA, galU, metL, methH, mviA, sodC, recA, recA, ssrA, ssrB, sirA, sirB, sirC, inv, hila, hilC, hild, rpoE, flgM, tonB, and slyA.
25. The genetically engineered bacterial cell according to claim 23 wherein the strain of bacteria is a strain of Salmonella.
26. The genetically engineered bacterial cell according to claim 25 wherein the strain of Salmonella is a strain of *S. typhi*.
27. The genetically engineered bacterial cell according to claim 26 wherein the one or more inactivating mutations are in a gene selected from the group consisting of a pab gene, a pur gene, an aro gene, asd, a dap gene, nadA, pncB, galE, pmi, fur, rpsL, ompR, htrA, hemA, cdt, cya, crp, dam, phoP, phoQ, rfc, poxA, galU, metL, methH, methH, mviA, sodC, recA, ssrA, ssrB, sirA, sirB, sirC, inv, hila, hilC, hild, rpoE, flgM, tonB, and slyA.

SYSTEM:OS - DIALOG OneSearch

File 155:MEDLINE(R) 1951-2004/Oct W5
(c) format only 2004 The Dialog Corp.
*File 155: Medline will stop updating COMPLETED records on November 17, 2004. Please see HELP NEWS 155 for details.

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File 35:Dissertation Abs Online 1861-2004/Oct
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File 94:JICST-EPlus 1985-2004/Oct W2
(c)2004 Japan Science and Tech Corp(JST)

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(c) 2004 The HW Wilson Co.

File 135:NewsRx Weekly Reports 1995-2004/Oct W5
(c) 2004 NewsRx

*File 135: New newsletters are now added. See Help News135 for the complete list of newsletters.

File 144:Pascal 1973-2004/Oct W5
(c) 2004 INIST/CNRS

File 149:TGG Health&Wellness DB(SM) 1976-2004/Oct W3
(c) 2004 The Gale Group

File 156:ToxFile 1965-2004/Oct W5
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*File 156: ToxFile now reloaded with 2004 MeSH.
Enter Help News156 for more information.

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(c) format only 2002 Dialog Corporation

*File 159: Cancerlit is no longer updating.
Please see HELP NEWS159.

File 162:Global Health 1983-2004/Sep
(c) 2004 CAB International

File 164:Allied & Complementary Medicine 1984-2004/Nov
(c) 2004 BLHCIS

File 172:EMBASE Alert 2004/Oct W5
(c) 2004 Elsevier Science B.V.

File 266:FEDRIP 2004/Aug
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(c) 2004 Reed Business Information Ltd.

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*File 370: This file is closed (no updates). Use File 47 for more current information.

File 399:CA SEARCH(R) 1967-2004/UD=14120
(c) 2004 American Chemical Society

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File 434:SciSearch(R) Cited Ref Sci 1974-1989/Dec
(c) 1998 Inst for Sci Info

File 444:New England Journal of Med. 1985-2004/Oct W5
(c) 2004 Mass. Med. Soc.

File 467:ExtraMED(tm) 2000/Dec
(c) 2001 Informania Ltd.

*File 467: F467 no longer updates; see Help News467.

Set Items Description

Cost is in DialUnits
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Set	Items	Description
S1	732	DNA?/TI AND ADENINE?/TI AND (METHYLASE? OR METHYLTRANSFERASE?)/TI
S2	296	S1/2000:2004
S3	436	S1 NOT S2
S4	172	RD (unique items)
S5	144	S3 AND (ATTENUAT? OR MUTANT? OR INSERT? OR DELET? OR TRANSPOS?)
S6	92	S5 AND (SALMON? OR COLI OR VIBRIO? OR PASTEUR? OR SHIGEL? OR NEISSERI?)

?t s6/9/1-14

6/9/1 (Item 1 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

(c) format only 2004 The Dialog Corp. All rts. reserv.

14504804 PMID: 10500219

DNA adenine methylase mutants of *Salmonella typhimurium* show defects in protein secretion, cell invasion, and M cell cytotoxicity.

Garcia-Del Portillo F; Pucciarelli M G; Casadesus J
Centro de Biologia Molecular "Severo Ochoa," Universidad Autonoma de Madrid-Consejo Superior de Investigaciones Cientificas, Cantoblanco, Madrid 28049, Spain.

Proceedings of the National Academy of Sciences of the United States of America (UNITED STATES) Sep 28 1999, 96 (20) p11578-83, ISSN 0027-8424 Journal Code: 7505876

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Mutants of *Salmonella typhimurium* lacking DNA adenine methylase are **attenuated** for virulence in BALB/c mice. LD(50) values of a DNA adenine methylation (Dam) (-) **mutant** are at least 10(3)- to 10(4)-fold higher than those of the parental strain when administrated by oral or intraperitoneal routes. Dam(-) **mutants** are unable to proliferate in target organs but persist in low numbers in these locations. Efficient protection to challenge with the virulent parental strain is observed in mice infected with a Dam(-) **mutant**. Use of the ileal loop assay shows that Dam(-) **mutants** are less cytotoxic to M cells and fail to invade enterocytes. In the tissue culture model, lack of DNA adenine methylation causes reduced ability to invade nonphagocytic cells. In contrast, no effect is observed either in intracellular proliferation within nonphagocytic cells or in survival within macrophages. The invasion defect of Dam(-) **mutants** is correlated with a distinct pattern of secreted proteins, which is observed in both PhoP(+) and PhoP(-) backgrounds. Altogether, our observations suggest a multifactorial role of Dam methylation in *Salmonella* virulence.

Tags: Female; Human; Support, Non-U.S. Gov't

Descriptors: Bacterial Proteins--secretion--SE; *Intestinal Mucosa
--microbiology--MI; **Salmonella typhimurium*--enzymology--EN;
*Site-Specific DNA-Methyltransferase (Adenine-Specific)--physiology--PH;
Animals; DNA Methylation; Hela Cells; Mice; Mice, Inbred BALB C; Mutation;
Salmonella typhimurium--metabolism--ME; *Salmonella typhimurium*
--pathogenicity--PY; Site-Specific DNA-Methyltransferase (Adenine-Specific)
--genetics--GE; Virulence

CAS Registry No.: 0 (Bacterial Proteins)

Enzyme No.: EC 2.1.1.72 (Site-Specific DNA-Methyltransferase (Adenine-Specific))

Record Date Created: 19991021

Record Date Completed: 19991021

6/9/2 (Item 2 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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13880569 PMID: 9575240

A temperature-sensitive DNA adenine methyltransferase mutant of Salmonella typhimurium.

Brawer R; Batista F D; Burrone O R; Sordelli D O; Cerquetti M C

Centro de Estudios Farmacologicos y Botanicos (CEFYO-CONICET) and University of Buenos Aires, School of Medicine, Serrano 669, 1414 Buenos Aires, Argentina.

Archives of microbiology (GERMANY) Jun 1998, 169 (6) p530-3, ISSN 0302-8933 Journal Code: 0410427

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

A temperature-sensitive mutant of *Salmonella typhimurium* was isolated earlier after **transposon** mutagenesis with Tn10d Tet. The **mutant** D220 grows well at 28 degreesC but has a lower growth rate and forms filaments at 37 degreesC. **Transposon** -flanking fragments of **mutant** D220 DNA were cloned and sequenced. The **transposon** was **inserted** in the *dam* gene between positions 803 and 804 (assigned allele number: *dam*-231 : : Tn10d Tet) and resulted in a predicted ten-amino-acid-shorter Dam protein. The **insertion** created a stop codon that led to a truncated Dam protein with a temperature-sensitive phenotype. The **insertion** *dam*-231 : : Tn10d Tet resulted in a *dam* "leaky" phenotype since methylated and unmethylated adenines in GATC sequences were present. In addition, the *dam*-231 : : Tn10d Tet **insertion** rendered *dam* **mutants** temperature-sensitive for growth depending upon the genetic background of the *S. typhimurium* strain. The wild-type *dam* gene of *S. typhimurium* exhibited 82% identity with the *Escherichia coli* *dam* gene.

Tags: Support, Non-U.S. Gov't

Descriptors: *Salmonella typhimurium*--enzymology--EN; *Site-Specific DNA-Methyltransferase (Adenine-Specific)--genetics--GE; DNA **Transposable Elements**--genetics--GE; Polymerase Chain Reaction; *Salmonella typhimurium*--genetics--GE; *Salmonella typhimurium* --growth and development--GD; Site-Specific DNA-Methyltransferase (Adenine-Specific)--isolation and purification--IP; Temperature

CAS Registry No.: 0 . (DNA Transposable Elements)

Enzyme No.: EC 2.1.1.- (Dam methyltransferase); EC 2.1.1.72 (Site-Specific DNA-Methyltransferase (Adenine-Specific))

Record Date Created: 19980713

Record Date Completed: 19980713

6/9/3 (Item 3 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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13209695 PMID: 8878670

DNA adenine methylase mutants of Salmonella typhimurium and a novel *dam*-regulated locus.

Torreblanca J; Casadesus J

Departamento de Genetica, Facultad de Biologia, Universidad de Sevilla, Spain.

Genetics (UNITED STATES) Sep 1996, 144 (1) p15-26, ISSN 0016-6731
Journal Code: 0374636

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Mutants of *Salmonella typhimurium* lacking DNA adenine methylase were isolated; they include **insertion and **deletion** alleles. The *dam* locus maps at 75 min between *cysG* and *aroB*, similar to the *Escherichia coli* *dam***

gene. **Dam- mutants** of *S. typhimurium* resemble those of *E. coli* in the following phenotypes: (1) increased spontaneous mutations, (2) moderate SOS induction, (3) enhancement of duplication segregation, (4) inviability of **dam recA** and **dam recB mutants**, and (5) suppression of the inviability of the **dam recA** and **dam recB** combinations by mutations that eliminate mismatch repair. However, differences between *S. typhimurium* and *E. coli* **dam mutants** are also found: (1) *S. typhimurium* **dam mutants** do not show increased UV sensitivity, suggesting that methyl-directed mismatch repair does not participate in the repair of UV-induced DNA damage in *Salmonella*. (2) *S. typhimurium* **dam recJ mutants** are viable, suggesting that the *Salmonella* RecJ function does not participate in the repair of DNA strand breaks formed in the absence of Dam methylation. We also describe a genetic screen for detecting novel genes regulated by Dam methylation and a locus repressed by Dam methylation in the *S. typhimurium* virulence (or "cryptic") plasmid.

Tags: Support, Non-U.S. Gov't

Descriptors: *Salmonella* typhimurium--enzymology--EN; *Site-Specific DNA-Methyltransferase (Adenine-Specific)--genetics--GE; Chromosome Mapping; Cloning, Molecular; DNA Methylation; DNA **Transposable** Elements; Gene **Deletion**; Genetic Complementation Test; Mutagenesis, **Insertional**; *Salmonella* typhimurium--genetics--GE; *Salmonella* typhimurium--radiation effects--RE; Site-Specific DNA-Methyltransferase (Adenine-Specific)--metabolism--ME; Ultraviolet Rays

CAS Registry No.: 0 (DNA Transposable Elements)

Enzyme No.: EC 2.1.1.- (Dam methyltransferase); EC 2.1.1.72 (Site-Specific DNA-Methyltransferase (Adenine-Specific))

Record Date Created: 19970128

Record Date Completed: 19970128

6/9/4 (Item 4 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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10004952 PMID: 8125341

The DNA adenine methyltransferase -encoding gene (dam) of *Vibrio cholerae*.

Bandyopadhyay R; Das J

Biophysics Division, Indian Institute of Chemical Biology, Calcutta.

Gene (NETHERLANDS) Mar 11 1994, 140 (1) p67-71, ISSN 0378-1119

Journal Code: 7706761

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The DNA adenine methyltransferase (MTase)-encoding gene (dam) of *Vibrio cholerae*, an organism belonging to the family **Vibrionaceae**, has been cloned and the complete nucleotide (nt) sequence determined. *V. cholerae* dam encodes a 21.5-kDa protein and is directly involved in methyl-directed DNA mismatch repair. It can substitute for the *Escherichia coli* enzyme and can suppress the phenotypic traits associated with *E. coli* **dam mutants**. Overproduction of *V. cholerae* Dam MTase does not result in hypermutability in either *V. cholerae* or *E. coli* cells. Overproduction of *V. cholerae* Dam in a pUC plasmid, however, fails to suppress the 2-aminopurine (2-AP)-sensitive phenotype of *E. coli* **dam mutants**. Homology between the nt and deduced amino acid (aa) sequences of the *E. coli* and *V. cholerae* dam genes is only 30-35%.

Tags: Support, Non-U.S. Gov't

Descriptors: Methyltransferases--genetics--GE; *Site-Specific DNA-Methyltransferase (Adenine-Specific); **Vibrio cholerae*--genetics--GE; Amino Acid Sequence; Base Sequence; Cloning, Molecular; DNA, Bacterial; *Escherichia coli*; Genetic Complementation Test; Genetic Vectors; Molecular Sequence Data; Recombinant Proteins--genetics--GE; *Vibrio cholerae*--enzymology--EN

Molecular Sequence Databank No.: GENBANK/X67820

CAS Registry No.: 0 (DNA, Bacterial); 0 (Genetic Vectors); 0 (Recombinant Proteins)

Enzyme No.: EC 2.1.1. (Methyltransferases); EC 2.1.1.- (Dam methyltransferase); EC 2.1.1.72 (Site-Specific DNA-Methyltransferase (Adenine-Specific))

Gene Symbol: dam

Record Date Created: 19940414

Record Date Completed: 19940414

6/9/5 (Item 5 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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09876948 PMID: 8226701

Analysis of the genetic requirements for viability of Escherichia coli K-12 DNA adenine methylase (dam) mutants .

Peterson K R; Mount D W

Department of Molecular and Cellular Biology, University of Arizona, Tucson 85721.

Journal of bacteriology (UNITED STATES) Nov 1993, 175 (22) p7505-8,

ISSN 0021-9193 Journal Code: 2985120R

Contract/Grant No.: GM24496; GM; NIGMS

Erratum in J Bacteriol 1994 Mar;176(5) 1554

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

RecBCD protein, necessary for Escherichia coli dam mutant viability, is directly required for DNA repair. Recombination genes recF+, recN+, recO+, and recQ+ are not essential for dam mutant viability; they are required for recBC sbcBC dam mutant survival. mutH, mutL, or mutS mutations do not suppress subinduction of SOS genes in dam mutants .

Tags: Support, U.S. Gov't, P.H.S.

Descriptors: Escherichia coli --enzymology--EN; *Escherichia coli --genetics--GE; *Methyltransferases--genetics--GE; *Site-Specific DNA-Methyltransferase (Adenine-Specific); Alleles; Exodeoxyribonuclease V; Exodeoxyribonucleases--genetics--GE; Exodeoxyribonucleases--metabolism--ME; Genes, Bacterial; Genotype; Methyltransferases--metabolism--ME; Rec A Recombinases--genetics--GE; Rec A Recombinases--metabolism--ME; Recombination, Genetic; SOS Response (Genetics); Suppression, Genetic

Enzyme No.: EC 2.1.1. (Methyltransferases); EC 2.1.1.- (Dam methyltransferase); EC 2.1.1.72 (Site-Specific DNA-Methyltransferase (Adenine-Specific)); EC 2.7.7.- (Rec A Recombinases); EC 3.1.- (Exodeoxyribonucleases); EC 3.1.11.5 (Exodeoxyribonuclease V); EC 3.1.11.5 (exodeoxyribonuclease V, E coli)

Gene Symbol: dam; lexA; recA; recB; recC; recF; recH; recN; recO; recQ; ryv; sula

Record Date Created: 19931214

Record Date Completed: 19931214

6/9/6 (Item 6 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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08550756 PMID: 2190555

Influence of DNA adenine methylase on the sensitivity of Escherichia coli to near-ultraviolet radiation and hydrogen peroxide.

Yallaly P; Eisenstark A

Division of Biological Sciences, University of Missouri, Columbia 65211.

Biochemical and biophysical research communications (UNITED STATES) May 31 1990, 169 (1) p64-9, ISSN 0006-291X Journal Code: 0372516

Contract/Grant No.: ESO4489; ES; NIEHS

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Near-ultraviolet (NUV) radiation and hydrogen peroxide (H2O2) inactivation studies were performed on *Escherichia coli* K-12 DNA adenine methylation (dam) mutants and on cells that carry plasmids which overexpress Dam methylase. Lack of methylation resulted in increased sensitivity to NUV and H2O2 (a photoproduct of NUV). In a dam mutant carrying a dam plasmid, the levels of Dam enzyme and resistance to NUV and H2O2 were restored. However, using a multicopy dam+ plasmid strain, increasing the methylase above wildtype levels resulted in an increase in sensitivity of the cells rather than resistance.

Tags: Support, Non-U.S. Gov't; Support, U.S. Gov't, P.H.S.

Descriptors: *Escherichia coli* --enzymology--EN; *Hydrogen Peroxide --toxicity--TO; *Site-Specific DNA-Methyltransferase (Adenine-Specific) --physiology--PH; *Ultraviolet Rays--adverse effects--AE; *Escherichia coli* --drug effects--DE; *Escherichia coli* --radiation effects--RE; Plasmids

CAS Registry No.: 0 (Plasmids); 7722-84-1 (Hydrogen Peroxide)

Enzyme No.: EC 2.1.1.72 (Site-Specific DNA-Methyltransferase (Adenine-Specific))

Record Date Created: 19900711

Record Date Completed: 19900711

6/9/7 (Item 7 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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08513379 PMID: 2185235

The DNA adenine methyltransferase (dam+) gene of bacteriophage T4 reverses the mutator phenotype of an *Escherichia coli* dam mutant.

Hall R M

Laboratory for Molecular Biology, CSIRO Division of Biotechnology, North Ryde, NSW, Australia.

Journal of bacteriology (UNITED STATES) May 1990, 172 (5) p2812-3,
ISSN 0021-9193 Journal Code: 2985120R

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The mutator phenotype of *Escherichia coli* dam mutants was found to be reversed by introduction of the bacteriophage T4 gene for DNA adenine methyltransferase. This precludes a direct role for the *E. coli* DNA adenine methyltransferase in mismatch repair, in addition to its role in strand discrimination, as suggested by earlier studies (S. L. Schlagman, S. Hattman, and M. G. Marinus, J. Bacteriol. 165:896-900, 1986).

Descriptors: *Escherichia coli* --genetics--GE; *Genes, Structural, Viral; *Methyltransferases--genetics--GE; *Mutation; *Site-Specific DNA-Methyltransferase (Adenine-Specific); *T-Phages--genetics--GE; Cloning, Molecular; *Escherichia coli* --enzymology--EN; Phenotype; Plasmids; T-Phages --enzymology--EN

CAS Registry No.: 0 (Plasmids)

Enzyme No.: EC 2.1.1. (Methyltransferases); EC 2.1.1.- (Dam methyltransferase); EC 2.1.1.72 (Site-Specific DNA-Methyltransferase (Adenine-Specific))

Record Date Created: 19900605

Record Date Completed: 19900605

6/9/8 (Item 8 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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08326251 PMID: 2510127

Single amino acid changes that alter the DNA sequence specificity of the DNA -[N6-adenine] methyltransferase (Dam) of bacteriophage T4.

Miner Z; Schlagman S L; Hattman S

Department of Biology, University of Rochester, NY 14627.

Nucleic acids research (ENGLAND) Oct 25 1989, 17 (20) p8149-57,
ISSN 0305-1048 Journal Code: 0411011
Contract/Grant No.: GM29227; GM; NIGMS
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS

Bacteriophage T4 codes for a DNA-[N6-adenine] methyltransferase (Dam) which recognizes primarily the sequence GATC in both cytosine- and hydroxymethylcytosine-containing DNA. Hypermethylating **mutants**, damh, exhibit a relaxation in sequence specificity, that is, they are readily able to methylate non-canonical sites. We have determined that the damh mutation produces a single amino acid change (Pro126 to Ser126) in a region of homology (III) shared by three DNA-adenine methyltransferases; viz, T4 Dam, Escherichia coli Dam, and the DpnII modification enzyme of Streptococcus pneumoniae. We also describe another **mutant**, damc, which methylates GATC in cytosine-containing DNA, but not in hydroxymethylcytosine-containing DNA. This mutation also alters a single amino acid (Phe127 to Val127). These results implicate homology region III as a domain involved in DNA sequence recognition. The effect of several different amino acids at residue 126 was examined by creating a polypeptide chain terminating codon at that position and comparing the methylation capability of partially purified enzymes produced in the presence of various suppressors. No enzyme activity is detected when phenylalanine, glutamic acid, or histidine is **inserted** at position 126. However, **insertion** of alanine, cysteine, or glycine at residue 126 produces enzymatic activity similar to Damh.

Tags: Support, U.S. Gov't, P.H.S.

Descriptors: DNA, Viral--genetics--GE; *Escherichia coli --genetics--GE; *Genes, Structural, Viral; *Mutation; *Proline; *Serine; *Site-Specific DNA-Methyltransferase (Adenine-Specific)--genetics--GE; *T-Phages--genetics--GE; Amino Acid Sequence; Base Sequence; Codon--genetics--GE; Escherichia coli --enzymology--EN; Kinetics; Molecular Sequence Data; Plasmids; Site-Specific DNA-Methyltransferase (Adenine-Specific) --isolation and purification--IP; Site-Specific DNA-Methyltransferase (Adenine-Specific) --metabolism--ME; T-Phages--enzymology--EN

CAS Registry No.: 0 (Codon); 0 (DNA, Viral); 0 (Plasmids); 147-85-3 (Proline); 56-45-1 (Serine)

Enzyme No.: EC 2.1.1.72 (Site-Specific DNA-Methyltransferase (Adenine-Specific))

Record Date Created: 19891204

Record Date Completed: 19891204

6/9/9 (Item 9 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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08102612 PMID: 3072268

The DNA [adenine -N6] methyltransferase (Dam) of bacteriophage T4.

Schlagman S L; Miner Z; Feher Z; Hattman S

Department of Biology, University of Rochester, NY 14627.

Gene (NETHERLANDS) Dec 20 1988, 73 (2) p517-30, ISSN 0378-1119

Journal Code: 7706761

Contract/Grant No.: GM-29227; GM; NIGMS

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

A functional bacteriophage T4 dam+ gene, which specifies a DNA [adenine-N6]methyltransferase (Dam), was cloned on a 1.8-kb HindIII fragment [Schlagman and Hattman, Gene 22 (1983) 139-156]. Sequence analysis [Macdonald and Mosig, EMBO J. 3 (1984) 2863-2871] revealed two overlapping in-phase open reading frames (ORFs). The 5' proximal ORF initiates translation at an AUG and encodes a 30-kDa polypeptide, whereas the

downstream ORF initiates translation at a GUG and encodes a 26-kDa polypeptide. Analysis of BAL 31 **deletions** in our original dam⁺ clone has verified that at least one of these overlapping ORFs, in fact, encodes T4 Dam. To investigate where T4 Dam translation is initiated, we have constructed plasmids in which a tac or lambda PL promoter is placed 5' to either the longer ORF or just the shorter ORF. Only clones which contain a promoter in front of the longer ORF produce active T4 Dam. This indicates that the 26-kDa polypeptide alone cannot be T4 Dam. Additional experiments suggest that only the 30-kDa polypeptide is required for enzyme activity and that the shorter ORF is not translated in plasmid-carrying cells. We also present evidence that T4 Dam is capable of methylating 5'-GATC-3', GATm5C, and GAThmC sequences; non-canonical sites (e.g., GACC) are also methylated, but much less efficiently.

Tags: Support, U.S. Gov't, P.H.S.

Descriptors: *Genes, Structural; *Genes, Viral; *Site-Specific DNA-Methyltransferase (Adenine-Specific)--genetics--GE; *T-Phages--genetics--GE; Cloning, Molecular; Escherichia coli --enzymology--EN; Escherichia coli --genetics--GE; Plasmids; Promoter Regions (Genetics); Recombinant Proteins--metabolism--ME; Saccharomyces cerevisiae--genetics--GE; Site-Specific DNA-Methyltransferase (Adenine-Specific)--metabolism--ME; T-Phages--enzymology--EN; Transformation, Genetic

CAS Registry No.: 0 (Plasmids); 0 (Recombinant Proteins)

Enzyme No.: EC 2.1.1.72 (Site-Specific DNA-Methyltransferase (Adenine-Specific))

Record Date Created: 19890605

Record Date Completed: 19890605

6/9/10 (Item 10 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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07870810 PMID: 2842672

A mutation in the DNA adenine methylase gene (dam) of Salmonella typhimurium decreases susceptibility to 9-aminoacridine-induced frameshift mutagenesis.

Ritchie L; Podger D M; Hall R M

CSIRO Division of Molecular Biology, North Ryde, NSW, Australia.

Mutation research (NETHERLANDS) Sep 1988, 194 (2) p131-41, ISSN 0027-5107 Journal Code: 0400763

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

A mutant of *Salmonella typhimurium* with a reduced response to mutation induction by 9-aminoacridine (9AA) has been isolated. The mutation (dam-2) is located in the DNA adenine methylase gene. The dam-2 mutant strain exhibits a level of sensitivity to 2-aminopurine (2AP) intermediate between that of the dam⁺ and the DNA adenine methylation-deficit dam-1 strain, and 2AP sensitivity was reversed by introduction of a mutH mutation or of the plasmid pMQ148 (which carries a functional *Escherichia coli* dam⁺ gene). However, the dam-2 strain is not grossly defective in DNA adenine methylase activity. Whole cell DNA appears full methylated at -GATC- sites. The levels of 9AA required to induce equivalent levels of frameshift mutagenesis in the dam-2 strain were approximately 2-fold higher than for the dam⁺ strain. Introduction of pMQ148 dam⁺ reduced the level of 9AA required for induction of frameshift mutations 4-fold in the dam-2 strain and 2-fold in the dam⁺ strain. The dam-2 mutation had no effect on the levels of ICR191 required for induction of frameshift mutations, but introduction of pMQ148 reduced the ICR191-induced mutagenesis 2-fold. The dam⁺/pMQ148, dam-2/pMQ148 and dam-1/pMQ148 strains showed identical dose-response curves for both 9AA and ICR191. These results are consistent with a slightly reduced (dam-2) or increased (pMQ148) rate of methylation at the replication fork. The 2AP sensitivity of the dam-2 strain cannot be simply explained. Furthermore, addition of methionine to the assay medium reverses the 2AP sensitivity of the dam-2 strain, but has no effect on 9AA

mutagenesis.

Descriptors: Aminacrine--pharmacology--PD; *Aminoacridines--pharmacology
--PD; *Genes, Bacterial; *Genes, Structural; *Methyltransferases--genetics
--GE; *Mutation; * **Salmonella** typhimurium--genetics--GE; DNA **Transposable**
Elements; Genotype; Microbial Sensitivity Tests; **Salmonella** typhimurium
--drug effects--DE; **Salmonella** typhimurium--enzymology--EN;
Site-Specific DNA-Methyltransferase (Adenine-Specific); Species Specificity
CAS Registry No.: 0 (Aminoacridines); 0 (DNA Transposable Elements);
90-45-9 (Aminacrine)
Enzyme No.: EC 2.1.1. (Methyltransferases); EC 2.1.1.72 (Site-Specific
DNA-Methyltransferase (Adenine-Specific))
Record Date Created: 19881004
Record Date Completed: 19881004

6/9/11 (Item 11 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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06951424 PMID: 3932821

**Viability of Escherichia coli K-12 DNA adenine methylase (dam)
mutants requires increased expression of specific genes in the SOS
regulon.**

Peterson K R; Wertman K F; Mount D W; Marinus M G
Molecular & general genetics - MGG (GERMANY, WEST) 1985, 201 (1)
p14-9, ISSN 0026-8925 Journal Code: 0125036
Contract/Grant No.: GM24496; GM; NIGMS; GM30330; GM; NIGMS
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS

We have examined the level of expression of the SOS regulon in cells
lacking DNA adenine methylase activity (dam-). Mud (Ap, lac) fusions to
several SOS operons (recA, lexA, uvrA, uvrB, uvrD, sulA, dinD and dinF)
were found to express higher levels of beta-galactosidase in dam- strains
than in isogenic dam+ strains. The attempted construction of dam- strains
that were also **mutant** in one of several SOS genes indicated that the
viability of methylase-deficient strains correlates with the inactivation
of the SOS repressor (LexA protein). Consistent with this, the wild-type
functions of two LexA-repressed genes (recA and ruv) appear to be required
for dam- strain viability.

Tags: Support, U.S. Gov't, Non-P.H.S.; Support, U.S. Gov't, P.H.S.

Descriptors: DNA Repair; *DNA, Bacterial--genetics--GE; *Escherichia
coli --genetics--GE; *Genes, Bacterial; *Genes, Structural;
*Methyltransferases--genetics--GE; *Mutation; Escherichia **coli**
--enzymology--EN; Escherichia **coli** --growth and development--GD; Genotype
; Rec A Recombinases--genetics--GE; Site-Specific DNA-Methyltransferase
(Adenine-Specific); Species Specificity; Transduction, Genetic;
beta-Galactosidase--genetics--GE

CAS Registry No.: 0 (DNA, Bacterial)
Enzyme No.: EC 2.1.1. (Methyltransferases); EC 2.1.1.72 (Site-Specific
DNA-Methyltransferase (Adenine-Specific)); EC 2.7.7.- (Rec A Recombinases)
; EC 3.2.1.23 (beta-Galactosidase)
Record Date Created: 19851218
Record Date Completed: 19851218

6/9/12 (Item 12 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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06194633 PMID: 6307815

**Molecular cloning of a functional dam+ gene coding for phage T4 DNA
adenine methylase.**

Schlagman S L; Hattman S

Gene (NETHERLANDS) May-Jun 1983, 22 (2-3) p139-56, ISSN 0378-1119

Journal Code: 7706761

Contract/Grant No.: GM-29227; GM; NIGMS

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Phages T2 and T4 induce synthesis of a DNA-adenine methylase which is coded for by a phage gene, *dam+*. These enzymes methylate adenine residues in specific sequences which include G-A-T-C, the methylation site of the host *Escherichia coli dam+* methylase. Methylation of G-A-T-C to G-m6A-T-C protects the site against cleavage by the MboI restriction nuclease. We have taken advantage of this property to enrich and screen for transformants which contain a cloned, functional T4 *dam+* gene. These recombinant molecules consist of a 1.85-kb HindIII fragment **inserted** into the plasmid pBR322; both orientations of the fragment express the methylase gene, suggesting that transcription is from a T4 promoter. We have tested the 1.85-kb **insert** for sensitivity to a variety of restriction nucleases and have found single sites for EcoRI, Ball, XbaI, and at least two sites for BstNI (EcoRII). The relative positions of these restriction sites have also been determined. Physical mapping was carried out by Southern blot hybridization with 32P-labeled (nick-translated clone) probe. These experiments showed that the **insert** corresponds to a HindIII fragment located on the physical map of T4 between positions 16.2 and 18.1 kb from the T4rIIA-rIIB junction. *E. coli dam-* possesses several phenotypic differences from the wild-type *dam+* parent, including an increased sensitivity to 2-aminopurine (2-AP). We found that T4 *dam+* clones could relieve *dam-* cells of their increased sensitivity to 2-AP.

Tags: Support, U.S. Gov't, P.H.S.

Descriptors: *Cloning, Molecular; *DNA (Cytosine-5-)-Methyltransferase --genetics--GE; *Genes, Structural; *Genes, Viral; *Methyltransferases --genetics--GE; *T-Phages--genetics--GE; DNA Restriction Enzymes; *Escherichia coli* --enzymology--EN; *Escherichia coli* --genetics--GE; Nucleic Acid Hybridization; Site-Specific DNA-Methyltransferase (Adenine-Specific); T-Phages--enzymology--EN
Enzyme No.: EC 2.1.1. (Methyltransferases); EC 2.1.1.37 (DNA (Cytosine-5-)-Methyltransferase); EC 2.1.1.72 (Site-Specific DNA-Methyltransferase (Adenine-Specific)); EC 3.1.21 (DNA Restriction Enzymes)

Record Date Created: 19830920

Record Date Completed: 19830920

6/9/13 (Item 13 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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06101268 PMID: 6300769

The isolation and characterization of the *Escherichia coli* DNA adenine methylase (*dam*) gene.

Brooks J E; Blumenthal R M; Gingeras T R

Nucleic acids research (ENGLAND) Feb 11 1983, 11 (3) p837-51, ISSN

0305-1048 Journal Code: 0411011

Contract/Grant No.: 5-R01-CA27275-02; CA; NCI; CA 09311-02; CA; NCI

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The *E. coli dam* (DNA adenine methylase) enzyme is known to methylate the sequence GATC. A general method for cloning sequence-specific DNA methylase genes was used to isolate the *dam* gene on a 1.14 kb fragment, **inserted** in the plasmid vector pBR322. Subsequent restriction mapping and subcloning experiments established a set of approximate boundaries of the gene. The nucleotide sequence of the *dam* gene was determined, and analysis of that sequence revealed a unique open reading frame which corresponded in length to that necessary to code for a protein the size of *dam*. Amino acid

composition derived from this sequence corresponds closely to the amino acid composition of the purified dam protein. Enzymatic and DNA:DNA hybridization methods were used to investigate the possible presence of dam genes in a variety of prokaryotic organisms.

Tags: Support, U.S. Gov't, Non-P.H.S.; Support, U.S. Gov't, P.H.S.

Descriptors: Cloning, Molecular; *DNA (Cytosine-5-)-Methyltransferase --genetics--GE; *DNA, Bacterial--isolation and purification--IP; *Escherichia coli --enzymology--EN; *Genes, Bacterial; *Genes, Structural; *Methyltransferases--genetics--GE; Amino Acid Sequence; Base Sequence; DNA Restriction Enzymes; DNA, Bacterial--genetics--GE; Nucleic Acid Hybridization; Plasmids

Molecular Sequence Databank No.: GENBANK/J01600

CAS Registry No.: 0 (DNA, Bacterial); 0 (Plasmids)

Enzyme No.: EC 2.1.1. (Methyltransferases); EC 2.1.1.37 (DNA (Cytosine-5-)-Methyltransferase); EC 3.1.21 (DNA Restriction Enzymes)

Record Date Created: 19830527

Record Date Completed: 19830527

6/9/14 (Item 14 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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04988009 PMID: 370403

In vitro methylation of bacteriophage lambda DNA by wild type (dam+) and mutant (damh) forms of the phage T2 DNA adenine methylase .

Brooks J E; Hattman S

Journal of molecular biology (ENGLAND) Dec 15 1978, 126 (3) p381-94, ISSN 0022-2836 Journal Code: 2985088R

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Tags: Support, U.S. Gov't, P.H.S.

Descriptors: *Coliphages--genetics--GE; *DNA (Cytosine-5-)-Methyltransferase; *DNA, Viral; *Methyltransferases; Base Sequence; DNA (Cytosine-5-)-Methyltransferase--genetics--GE; Escherichia coli --genetics --GE; Methylation; Methyltransferases--genetics--GE; Mutation; Transfection

CAS Registry No.: 0 (DNA, Viral)

Enzyme No.: EC 2.1.1. (Methyltransferases); EC 2.1.1.37 (DNA (Cytosine-5-)-Methyltransferase)

Record Date Created: 19790516

Record Date Completed: 19790516

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Status: Signed Off. (1 minutes)